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1. (Amended) A method of determining the risk of the recurrence of colorectal cancer for a subject using a Genomic Damage Fraction, comprising:

a. determining the relative change in quantity of nucleic acids between cancerous cells and non-cancerous cells of said subject;

b. determining the Genomic Damage Fraction from the results of step (a)

c. determining the prognosis of said subject according to said subject's GDF, where a GDF greater than a predetermined GDF is indicative of a first clinical outcome, and a GDF lesser than a predetermined GDF is indicative of a second clinical outcome, wherein said clinical outcome comprises risk of the recurrence of colorectal cancer.

13. (Amended) A method of determining the likelihood that colorectal cancer will become metastatic for a subject with colorectal cancer, comprising:

a. generating the AP-PCR DNA fingerprint of non-cancerous cells from said subject;

b. generating the AP-PCR DNA fingerprint of primary cancer cells from said subject; and

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b2 cix
c. identifying chromosomal regions from AP-PCR DNA fingerprint data of steps (a), (b) and (c) wherein the occurrence of chromosome 6 gains or chromosome 4 losses is prognostic of metastasis for said colorectal cancer.

17. (Amended) A method of prognosing survival for a subject with colorectal cancer, comprising:

a. generating the AP-PCR DNA fingerprint of non-cancerous cells from said subject;

b. generating the AP-PCR DNA fingerprint of primary cancer cells from said subject;

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c. identifying chromosomal regions from AP-PCR DNA fingerprint data of steps (a) and (b), where gains or losses of nucleic acids occur; and

d. comparing said AP-PCR DNA fingerprints from step a and step b wherein chromosome 4 loss is prognostic of poor survival for said subject.

19. (Amended) A method of predicting the likelihood that colorectal cancer will become metastatic for a subject with colorectal cancer using an amplotype from said subject, comprising:

b4
a. locating chromosomal regions that have gained and lost nucleic acids using AP-PCR DNA fingerprinting;

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b. identifying said chromosomal regions that have lost nucleic acids; and

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c. identifying said chromosomal regions that have gained nucleic acids;

wherein the combination of chromosome 6 gains and chromosome 4 losses are prognostic of metastasis for said colorectal cancer.

20. (Amended) The method of claim 19, wherein the results of step (b) and step (c) are displayed where said gains and losses of nucleic acids are listed according to the chromosomal regions where they occur, wherein the combination of gains and losses according to chromosomal regions are prognostic of metastasis for said colorectal cancer.

bs
21. (Amended) A method of identifying a genomic region relevant for colorectal cancer in a subject having colorectal cancer, comprising:

(a) generating the AP-PCR DNA fingerprint of non-cancerous cells, primary cancer, and metastatic tumor cells from said subject; and

(b) identifying said genomic regions from AP-PCR DNA fingerprint data of step (a), showing gains and losses of nucleic acids in certain genomic regions, thereby identifying a genomic region linked to a colorectal cancer gene.
